

Genetic population structure and connectivity of the big blue octopus, *Octopus cyanea* (Gray, 1849), in the Western Indian Ocean

Van Nieuwenhove Annelore H. M., A. Ratsimbazafy Hajaniaina and Kochzius Marc

Marine Biology, DBIO, Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussels, Belgium

E-mail: Annelore.Van.Nieuwenhove@vub.be

For many communities along the East African coast and islands of the Western Indian Ocean (WIO), artisanal octopus fishing is a very important economic and subsistence activity. In the recent decades, these artisanal African octopus fisheries have grown tremendously due to an increasing market demand for cephalopods worldwide and have shifted their focus from local and inland consumption to international export markets. However, these drastically increasing exploitation rates cause concern over sustainability of *Octopus cyanea* populations, the commercially most important octopus species in the WIO. To maintain the sustainability of these considerable socio-economic important octopus populations, management actions have to be taken, including the establishment of permanent Marine Protected Areas (MPAs). MPAs have been widely used to control overexploitation, to protect genetic diversity and have shown to be effective in increasing the biomass of marine stocks, both within and outside the protected area. When designing networks of MPAs, connectivity among populations through larval dispersal is a crucial factor which should be considered, since it determines gene flow, genetic diversity and genetic population structure, as well as the ability to persist and recover from stressors like overfishing.

This study determines the connectivity and genetic structure of *O. cyanea* populations in the WIO, using the mitochondrial cytochrome C oxidase subunit 1 (COI) gene as marker. Arm tips of 302 individuals of *O. cyanea* were collected on landing sites and markets, at 15 different sites in Madagascar, Tanzania and Kenya. DNA was extracted and the universal primers HCO2198 (5'-TAA ACT TCA GGG TGA CCA AAA AAT CA-3') and LCO1490 (5'-GGT CAA CAA ATC ATA AAG ATA TTG G-3'), were used for the amplification.

The aim is to provide an answer to the following questions: is a genetic break present between the populations of Madagascar and the African mainland? Is there gene flow among the coast of Madagascar? Are the results comparable when using microsatellite markers? To our knowledge, this will be the first study worldwide dealing with population genetics of *O. cyanea*. Therefore, findings from this study are pioneering and can be used to further expand the knowledge base available for marine management decisions in the WIO.

Keywords: Marine Protected Area; population genetics; gene flow; mitochondrial DNA; COI; Madagascar